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## **RAW SEQUENCE LISTING ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/595,526

Source: 1645

Date Processed by STIC: 9-6-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

SEP 28 2001

TECH CENTER 1600/2900

M. Rao

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/595,526

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence-Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>-Organism (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>-Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>-Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>-ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Re-run

1645

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000  
 TIME: 11:05:03

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 Output Set: N:\CRF3\09062000\I595526.raw

5 <110> APPLICANT: Lawn, Richard M.  
 7 Wade, David  
 9 Garvin, Michael  
 11 Oram, John F.  
 15 <120> TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol  
 17 Efflux and Raising HDL using ATP Binding Cassette  
 19 Transporter Protein ABC1  
 23 <130> FILE REFERENCE: 99,395-A  
 C--> 27 <140> CURRENT APPLICATION NUMBER: US/09/595,526  
 C--> 29 <141> CURRENT FILING DATE: 2000-06-16  
 33 <150> PRIOR APPLICATION NUMBER: US 60/140,264  
 35 <151> PRIOR FILING DATE: 1999-06-18  
 39 <150> PRIOR APPLICATION NUMBER: US 60/153,872  
 41 <151> PRIOR FILING DATE: 1999-08-14  
 45 <150> PRIOR APPLICATION NUMBER: US 60/166,573  
 47 <151> PRIOR FILING DATE: 1999-11-19  
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Does Not Comply  
 Corrected Diskette Needed

See p. 4, 5

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000  
TIME: 11:05:03

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/595,526

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000  
TIME: 11:05:03

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365 tttctagtca gtaaacattt gtaaaaatac tgtttcacta atacttactg ttaactgtct 8880
367 tgagagaaaa gaaaaaatat agagaaactat tgtttgggga agttcaaagt atctttcaat 8940
369 atcattacta acttcttcca ctttttccaa aatttgaaata ttaacgctaa aggtgtaaga 9000
371 ctccagattt caaattaatc tttctatatt ttttaaaatt acagaatatt atataacca 9060
373 ctgctgaaaa agaaaaaaat gattgtttta gaagttaaag tcaatattga ttttaaat 9120
375 aagtaaatgaa ggcataattc caataactag tgatatggca tegtgtgcaat ttacagtatc 9180
377 ttcaaaaata cagaatttat agaataattt ctccctcattt aatatttttc aaaaacaaag 9240
379 ttatggtttc ctcatcttac taaaaatcga ttctaattct tcattatagt aaatctatga 9300
381 gcaactcctt acttcggttc ctctgatttc aaggccatat tttaaaaaat caaaaggcac 9360
383 tgtgaactat tttgaagaaa acacgacatt ttaatacaga ttgaaaggac ctctctgaa 9420
385 gctagaaaaa atctatagtt atacatcttc attaatactg tgttaccttt taaaatagta 9480
387 attttttaca ttttctgtg taaacctaat tgtggtagaa atttttacca actctatact 9540
389 caatcaagca aattttctgt atattccctg tggaaatgac ctatgtgagt ttcagaaatt 9600
391 ctcaaaatac gtgttcaaaa attttctgct ttgcactttt gggacacctc agaaaactta 9660
393 ttaacaactg tgaatatgag aaatacagaa gaaaataata agccctctat acataaatgc 9720
395 ccagcacaaat tcattgttaa aaaacaacca aacctcacac tactgtattt cattatctgt 9780
397 actgaaagca aatgctttgt gactattaaa tgttgccatc cattcattca ctgtatagta 9840
W--> 399 atcattgact aaagccattt gctgtgtttt cttctgtgtg cttctatatt caggtaaaat 9900
401 attttccaaa gagccatgtg tcatgtaata ctgaaccctt tgatattgag acattaattt 9960
W--> 403 ggacccttgg tattatctac tagaataatg taataactnn gaaatattgc tctaattctt 10020
W--> 405 tcaaaatggg ccatccccc taaaanyttc tattttccata aggatttagc ttgcttatcc 10080
407 cttctttata ccataagatga agctgttttt gtgctctttt ttcatcattg gccctcatc 10140
409 caagcacttt acgctgtctg taatgggac tatttttgca ctggaatata tgagaattgc 10200
411 aaaactagac aaaagtttca caacagattt ctaagttaaa tcattttcat taaaaggaaa 10260

```

<220> blank line  
<221> name/key  
<222> location  
<223> other info.

Missing mandatory  
<220> to <223> features  
to explain "n's" in  
Sequence. See  
#10 on Error  
Summary Sheet.

This error has  
been indicated  
elsewhere in the  
sequence listing. Please  
check and correct.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000  
TIME: 11:05:03

Input-Set: A:\CVT 158.txt  
Output-Set: N:\CRF3\09062000\I595526.raw

```

413 aaagaaaaaa-aattttgtat-gtcaataact ttatatgaag tattaaaaatg catatttcta 10320
415 tgttgtaata taatgagtca caaaataaag ctgtgacagt tctgttaaaa aaaaaaaaaa 10380
417 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 10440
419 aa
422 <210> SEQ ID NO: 2
424 <211> LENGTH: 2261
426 <212> TYPE: PRT
428 <213> ORGANISM: Homo sapiens
432 <400> SEQUENCE: 2
434 Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Trp Lys Asn Leu Thr
436 1 5 10 15
440 Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
442 20 25 30
446 Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
448 35 40 45
452 Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
454 50 55 60
458 Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
460 65 70 75 80
464 Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
466 85 90 95
470 Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
472 100 105 110
476 Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
478 115 120 125
482 Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Asn Leu Lys Leu
484 130 135 140
488 Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly Phe Leu Tyr His
490 145 150 155 160
494 Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met Leu Arg Ala Asp
496 165 170 175
500 Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln Leu His Leu Thr
502 180 185 190
506 Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile Gln Leu Gly Asp
508 195 200 205
512 Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Lys Glu Lys Leu Ala Ala
514 210 215 220
518 Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu Lys Pro Ile Leu
520 225 230 235 240
524 Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys Glu Leu Ala Glu
526 245 250 255
530 Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu Ala Gln Glu Leu
532 260 265 270
536 Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu Val Met Phe Leu
538 275 280 285
542 Thr Asn Val Asn Ser Ser Ser Ser Ser Thr Gln Ile Tyr Gln Ala Val
544 290 295 300
548 Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly Leu Lys Ile Lys
550 305 310 315 320

```

← F.Y.I.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000

TIME: 11:05:04

Input Set : A:\CVT 158.txt

Output Set: N:\CRF3\09062000\I595526.raw

L:27 M:270 C: Current Application Number differs, Replaced Application Number  
L:29 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:399 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1  
L:399 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:399 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:399 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:399 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1  
L:403 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1  
L:403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
M:340 Repeated in SeqNo=1  
L:405 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1  
L:405 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:405 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:1368 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:1368 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:1368 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:1368 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:1368 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
L:1370 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:1370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:1370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:1370 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
M:340 Repeated in SeqNo=4  
L:1372 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:1372 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:1372 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:1372 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:1374 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:1374 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:1374 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:1374 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:1580 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6  
L:1580 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:1580 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:1580 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:1580 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
L:1584 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6  
L:1584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:1584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:1584 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
M:340 Repeated in SeqNo=6  
L:1586 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6  
L:1586 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:1586 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:1586 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000  
TIME: 11:05:04

Input Set : A:\CVT 158.txt  
Output Set: N:\CRF3\09062000\I595526.raw

L:1945 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:1945 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:1945 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:1945 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:1945 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7  
L:1949 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:1949 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:1949 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:1949 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
M:340 Repeated in SeqNo=7  
L:3173 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9  
L:3173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9  
L:3173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9  
M:340 Repeated in SeqNo=9